SEQUENCE LISTING

<110> SIEMEISTER, GERHARD
       HABEREY, MARTIN
       THIERAUCH, KARL-HEINZ

<120> COMBINATIONS AND COMPOSITIONS WHICH INTERFERE WITH
       VEGF/VEGF AND ANGIOPOIETIN/TIE RECEPTOR FUNCTION
       AND THEIR USE

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<140> 09/887,527
<141> 2001-06-25

<150> DE 00250194.8
<151> 2000-06-23

<150> DE 00250214.4
<151> 2000-06-28

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<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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<213> Homo sapiens

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<210> 26
<211> 689
<212> DNA
<213> Homo sapiens

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<210> 27
<211> 471
<212> DNA
<213> Homo sapiens

<400> 27
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<210> 28
<211> 929
<212> DNA
<213> Homo sapiens

<400> 28
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gattccaccc cagccctggt acaagtctac tgtcatccac atgactgttg gaggcttcct 240
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<210> 29
<211> 1775
<212> DNA
<213> Homo sapiens

<400> 29
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gccccaccacc aagctggtga aggagctgcg gcccc                            1775
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<210> 30
<211> 1546
<212> DNA
<213> Homo sapiens
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<400> 30
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acaccatcta cgggcaccat ggaactgctt caagtgacca ttctttttct tctgcccagt 180
atttgcagca gtaacagcac aggtgtttta gaggcagcta ataattcact tgttgttact 240
acaacaaaac catctataac aacaccaaac acagaatcat tacagaaaaa tgttgtcaca 300
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atgtcaacag ctactttttt aacaagtaaa gatgaaggat tgaaagccac aaccactgat 420
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<210> 31
<211> 750
<212> DNA
<213> Homo sapiens
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ggattggaaa acggtgttta aagagaagag aacattttaa cataaatgtc attaagaatc 720
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<210> 32
<211> 1620
<212> DNA
<213> Homo sapiens

<400> 32
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ctgaggtctt ttggaagata atgtagaaaa ccactaccta ttgaaggcct gttttggcta  180
atctgtgcaa actctgatga tacctgcctt atgtggattc ttttccacac tgctttcatt  240
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acatacagca ttgtacatta caatgaaaat gtgtaactta agggtattat atatataaat  1560
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<210> 33
<211> 2968
<212> DNA
<213> Homo sapiens

<400> 33
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gaaagtgaag gcagtgaagg tgatgaggaa gatgaaaagg tgtcagatga gaaggattca  180
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cggcgacttg aacatagtaa aaatgtaaac accgaaaagc taagagcccc tattatctgc  360
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<210> 34
<211> 6011
<212> DNA
<213> Homo sapiens

<400> 34
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<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens


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<211> 956
<212> DNA
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<211> 536
<212> DNA
<213> Homo sapiens

<400> 43
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<212> DNA
<213> Homo sapiens

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<211> 169
<212> DNA
<213> Homo sapiens

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<210> 46
<211> 769
<212> DNA
<213> Homo sapiens

<400> 46
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<213> Homo sapiens

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<213> Homo sapiens

<400> 48

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<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<210> 51
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<212> DNA
<213> Homo sapiens

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<213> Homo sapiens

<400> 52
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<211> 2270
<212> DNA
<213> Homo sapiens

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aagatggtga agggtgggat ggatgaggag cgtggtgacg ggggcctgca gcgggttggg 1620
gaccctgtgc tgcgtt                                                  1636

<210> 57
<211> 460
<212> DNA
<213> Homo sapiens

<400> 57
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tggaatgagc taaagcagcc gcctgggggtg ggaggccgag cccatttgta tgcagcaggg 180
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atgcccgcag agccctccct cacactccat cctgtccagc cctaattgtg caggtgggga 300
aactgaggct gggaagtcac atagcaagtg actggcagag ctgggactgg aacccaacca 360
gcctcctaga ccacggttct tcccatcaat ggaatgctag agactccagc caggtgggta 420
ccgagctcga attcgtaatc atggtcatag ctgtttcctg                        460

<210> 58
<211> 1049
<212> DNA
<213> Homo sapiens

<400> 58
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tgacgacatg ctggctcaca ttttgcagtt ctgcagaagt cccccctccca gcctggacta 180
cagcagcact ttcccgtggg ggtgcagtag ccgtttcgac agagcctgga gcactctgaa 240
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ggatctacaa ttttgtagag ttttccattg tgagtctggg tcatactttt actgcttgat 360
aaaatgtaaa cttcacctag ttcatcttct ccaaatccca agatgtgacc ggaaaagtag 420
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```
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ggcacgttgc acatgtctgt gtccacatcc agccgtagca ctgagcctgt gaaatcactt 900
aacccatcca tttcttccat atcatccagt gtaatcatcc catcaccaag aatgatgtac 960
aaaaacccgt cagggccaaa gagcagttgc cctcccagat gctttctgtg gagttctgca 1020
acttcaagaa agactctggc tgttctcaa                                  1049
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<210> 59
<211> 747
<212> DNA
<213> Homo sapiens

<400> 59
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ccttaattta caaagcctca gtcattcata cacattaggg gatccacagt gttcaaggaa 120
cttaaatata atgtatcata ccaacccaag taaaccaagt acaaaaaata ttcatataaa 180
gttgttcaca cgtaggtcct agattaccag cttctgtgca aaaaaaggaa atgaagaaaa 240
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ctcgtctgtc ccacacaaat gtttaagaag tcactgcaat gtactccccg gctctgatga 360
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gctctcctag aaaaccagcg ggacggcctc cctgctgata ccgtctataa ccttagggg 480
ccctcgggca ggcaacggca gtggactcat ctcggtgatg gctgtagatg ctaacactgg 540
ccaattcaat gccacaccta ctggttaccc tttgagggca tttctccaga cagaagcccc 600
ttgaagccta ggtagggcag gatcagagat acaccgtgt ttgtctcgaa gggctcccaca 660
gcccagtacg acatgcttgc agaagtagta tctctggact tctgcctcca gtcgaccggc 720
cgcgaattta gtagtaatag cggccgc                                    747
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<210> 60
<211> 1036
<212> PRT
<213> Homo sapiens

<400> 60
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Met Tyr Leu Val Ala Gly Asp Arg Gly Leu Ala Gly Cys Gly His Leu
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Leu Val Ser Leu Leu Gly Leu Leu Leu Pro Ala Arg Ser Gly Thr
             20                  25                  30

Arg Ala Leu Val Cys Leu Pro Cys Asp Glu Ser Lys Cys Glu Glu Pro
         35                  40                  45

Arg Asn Arg Pro Gly Ser Ile Val Gln Gly Val Cys Gly Cys Cys Tyr
     50                  55                  60

Thr Cys Ala Ser Gln Gly Asn Glu Ser Cys Gly Gly Thr Phe Gly Ile
 65                  70                  75                  80

Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu
                 85                  90                  95
```

```
Asn Gly Asp Ser Leu Thr Glu Tyr Glu Ala Gly Val Cys Glu Asp Glu
        100             105             110

Asn Trp Thr Asp Asp Gln Leu Leu Gly Phe Lys Pro Cys Asn Glu Asn
        115             120             125

Leu Ile Ala Gly Cys Asn Ile Ile Asn Gly Lys Cys Glu Cys Asn Thr
130             135             140

Ile Arg Thr Cys Ser Asn Pro Phe Glu Phe Pro Ser Gln Asp Met Cys
145             150             155             160

Leu Ser Ala Leu Lys Arg Ile Glu Glu Glu Lys Pro Asp Cys Ser Lys
                165             170             175

Ala Arg Cys Glu Val Gln Phe Ser Pro Arg Cys Pro Glu Asp Ser Val
            180             185             190

Leu Ile Glu Gly Tyr Ala Pro Pro Gly Glu Cys Cys Pro Leu Pro Ser
            195             200             205

Arg Cys Val Cys Asn Pro Ala Gly Cys Leu Arg Lys Val Cys Gln Pro
    210             215             220

Gly Asn Leu Asn Ile Leu Val Ser Lys Ala Ser Gly Lys Pro Gly Glu
225                 230             235                 240

Cys Cys Asp Leu Tyr Glu Cys Lys Pro Val Phe Gly Val Asp Cys Arg
            245             250             255

Thr Val Glu Cys Pro Thr Val Gln Gln Thr Ala Cys Pro Pro Asp Ser
            260             265             270

Tyr Glu Thr Gln Val Arg Leu Thr Ala Asp Gly Cys Cys Thr Leu Pro
        275             280             285

Thr Arg Cys Glu Cys Leu Ser Gly Leu Cys Gly Phe Pro Val Cys Glu
    290             295             300

Val Gly Ser Thr Pro Arg Ile Val Ser Arg Gly Asp Gly Thr Pro Gly
305             310             315             320

Lys Cys Cys Asp Val Phe Glu Cys Val Asn Asp Thr Lys Pro Ala Cys
            325             330             335

Val Phe Asn Asn Val Glu Tyr Tyr Asp Gly Asp Met Phe Arg Met Asp
        340             345             350

Asn Cys Arg Phe Cys Arg Cys Gln Gly Gly Val Ala Ile Cys Phe Thr
        355             360             365

Ala Gln Cys Gly Glu Ile Asn Cys Glu Arg Tyr Tyr Val Pro Glu Gly
    370             375             380

Glu Cys Cys Pro Val Cys Glu Asp Pro Val Tyr Pro Phe Asn Asn Pro
385             390             395             400
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Ala Gly Cys Tyr Ala Asn Gly Leu Ile Leu Ala His Gly Asp Arg Trp
            405   410   415

Arg Glu Asp Asp Cys Thr Phe Cys Gln Cys Val Asn Gly Glu Arg His
            420   425   430

Cys Val Ala Thr Val Cys Gly Gln Thr Cys Thr Asn Pro Val Lys Val
            435   440   445

Pro Gly Glu Cys Cys Pro Val Cys Glu Glu Pro Thr Ile Ile Thr Val
    450   455   460

Asp Pro Pro Ala Cys Gly Glu Leu Ser Asn Cys Thr Leu Thr Arg Lys
465   470   475   480

Asp Cys Ile Asn Gly Phe Lys Arg Asp His Asn Gly Cys Arg Thr Cys
            485   490   495

Gln Cys Ile Asn Thr Gln Glu Leu Cys Ser Glu Arg Lys Gln Gly Cys
            500   505   510

Thr Leu Asn Cys Pro Phe Gly Phe Leu Thr Asp Ala Gln Asn Cys Glu
            515   520   525

Ile Cys Glu Cys Arg Pro Arg Pro Lys Lys Cys Arg Pro Ile Ile Cys
    530   535   540

Asp Lys Tyr Cys Pro Leu Gly Leu Leu Lys Asn Lys His Gly Cys Asp
545   550   555   560

Ile Cys Arg Cys Lys Lys Cys Pro Glu Leu Ser Cys Ser Lys Ile Cys
            565   570   575

Pro Leu Gly Phe Gln Gln Asp Ser His Gly Cys Leu Ile Cys Lys Cys
            580   585   590

Arg Glu Ala Ser Ala Ser Ala Gly Pro Pro Ile Leu Ser Gly Thr Cys
            595   600   605

Leu Thr Val Asp Gly His His His Lys Asn Glu Glu Ser Trp His Asp
    610   615   620

Gly Cys Arg Glu Cys Tyr Cys Leu Asn Gly Arg Glu Met Cys Ala Leu
625   630   635   640

Ile Thr Cys Pro Val Pro Ala Cys Gly Asn Pro Thr Ile His Pro Gly
            645   650   655

Gln Cys Cys Pro Ser Cys Ala Asp Asp Phe Val Val Gln Lys Pro Glu
            660   665   670

Leu Ser Thr Pro Ser Ile Cys His Ala Pro Gly Gly Glu Tyr Phe Val
            675   680   685

Glu Gly Glu Thr Trp Asn Ile Asp Ser Cys Thr Gln Cys Thr Cys His
    690   695   700

Ser Gly Arg Val Leu Cys Glu Thr Glu Val Cys Pro Pro Leu Leu Cys
705   710   715   720

Gln Asn Pro Ser Arg Thr Gln Asp Ser Cys Cys Pro Gln Cys Thr Asp
                725   730   735

Gln Pro Phe Arg Pro Ser Leu Ser Arg Asn Asn Ser Val Pro Asn Tyr
            740   745   750

Cys Lys Asn Asp Glu Gly Asp Ile Phe Leu Ala Ala Glu Ser Trp Lys
        755   760   765

Pro Asp Val Cys Thr Ser Cys Ile Cys Ile Asp Ser Val Ile Ser Cys
    770   775   780

Phe Ser Glu Ser Cys Pro Ser Val Ser Cys Glu Arg Pro Val Leu Arg
785   790   795   800

Lys Gly Gln Cys Cys Pro Tyr Cys Ile Lys Asp Thr Ile Pro Lys Lys
            805   810   815

Val Val Cys His Phe Ser Gly Lys Ala Tyr Ala Asp Glu Glu Arg Trp
            820   825   830

Asp Leu Asp Ser Cys Thr His Cys Tyr Cys Leu Gln Gly Gln Thr Leu
    835   :   840   845

Cys Ser Thr Val Ser Cys Pro Pro Leu Pro Cys Val Glu Pro Ile Asn
    850   855   860

Val Glu Gly Ser Cys Cys Pro Met Cys Pro Glu Met Tyr Val Pro Glu
865   870   875   880

Pro Thr Asn Ile Pro Ile Glu Lys Thr Asn His Arg Gly Glu Val Asp
            885   890   895

Leu Glu Val Pro Leu Trp Pro Thr Pro Ser Glu Asn Asp Ile Val His
        900   905   910

Leu Pro Arg Asp Met Gly His Leu Gln Val Asp Tyr Arg Asp Asn Arg
    915   920   925

Leu His Pro Ser Glu Asp Ser Ser Leu Asp Ser Ile Ala Ser Val Val
    930   935   940

Val Pro Ile Ile Ile Cys Leu Ser Ile Ile Ile Ala Phe Leu Phe Ile
945   950   955   960

Asn Gln Lys Lys Gln Trp Ile Pro Leu Leu Cys Trp Tyr Arg Thr Pro
            965   970   975

Thr Lys Pro Ser Ser Leu Asn Asn Gln Leu Val Ser Val Asp Cys Lys
        980   985   990

Lys Gly Thr Arg Val Gln Val Asp Ser Ser Gln Arg Met Leu Arg Ile
        995   1000   1005

Ala Glu Pro Asp Ala Arg Phe Ser Gly Phe Tyr Ser Met Gln Lys Gln
    1010   1015   1020

Asn His Leu Gln Ala Asp Asn Phe Tyr Gln Thr Val
1025   1030   1035